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Web service for automated detection and analysis of radiation-induced foci in cell nuclei

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This work was carried out within the framework of a joint project between MLIT and LRB JINR to create an information system for automating the analysis of radiobiological experiments.

Among the various types of radiation-induced DNA damage, the most crucial and dangerous types are DNA double-strand breaks (DSBs). To visualize DNA DSBs, the immunofluorescence staining method is used, which is based on the detection of specific protein markers involved in the process of DNA DSB repair where proteins accumulate at the sites of DNA DSB occurrence, forming radiation-induced foci (RIF). The number of RIF is typically assessed by visual inspection. However, manual scoring is a time-consuming work and prone to human error.

To automate the RIF analysis, we have followed a deep learning approach which consists of two stages; first a pretarained neural network called SAM2 is used to detect the cells in each image, then the trained neural network YOLO (You-Only-Look-Once) on our foci-annotated data is used to detect foci in each cell. Based on this model, we have developed a web service on the Writer Framework. The web service allows the user to observe the identified cells in the uploaded fluorescent image, choose the desired cells, automatically get the marked foci in each cell image and receive the numerical tables which include an assessment of the cell area, the number of RIF per cell and the average number of RIF in the image. The web service was developed and deployed on the basis of the ML/DL/HPC ecosystem of the heterogeneous HybriLIT platform and is available on the website https://mostlit.jinr.ru .

Keywords: Web service, deep learning, data analysis, DNA double-strand breaks, radiation-induced foci, radiobiology.

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